

Entrez Tutorial

NCBI's Entrez is an integrated, text-based search and retrieval system for more than 30 biologically-oriented databases. Entrez provides links to related records within the same database and between other databases in Entrez. This course will demonstrate how to:

- Obtain information about various database entries
- Search databases effectively using features such as Limits, Preview/Index and History
- Filter search results
- Highlight search terms
- Access, download and save records in various formats
- Access related entries in the database and other databases
- Save search strategies and results
- Retrieve large amounts of data as a batch
- Select an option to automatically update and e-mail search results

These are some of the examples of searches you will be able to perform after participating in this exercise:

- an organism and obtain its available data from the Entrez databases such as the genome sequence, proteins and their homologs, expressed sequences, Single Nucleotide Polymorphisms, etc.
- genes expressed in a particular tissue
- homologs among the annotated genes of several completely sequenced eukaryotic genomes
- aligned sequences from a population, phylogenetic, or mutation study
- SNPs on a certain chromosome that change amino acid sequence and have clinical associations
- articles that have free full text access

This course will cover databases such as PubMed, PubMed Central (PMC), Taxonomy, PopSet, OMIM, Homologene, Unigene, and the Single Nucleotide Polymorphism database (dbSNP). Some of the other databases are covered in other tutorials such as GenBank and Gene.

The following handout includes screenshots of the first exercise.

Exercise 1:

I. PubMed, PMC, Taxonomy and PopSet

Perform a search for mammoth across all of the Entrez databases. Which databases contain records associated with the term mammoth? Link to the mammoth literature citations in the PubMed database. Identify the articles available free in PMC. Access the article “The year of the mammoth”. What are the cited articles in this publication? Download the abstracts of these articles. How many of them are available free in PMC? Access publications of some of the authors of these articles.

Go back to the mammoth search in Pubmed. Display the PopSet links. Access the record by Greenwood with PopSet ID 14090839. View the alignment in various formats. Link from the record to the Nucleotide database. The sequence alignment of which gene is studied in this PopSet? Display the Taxonomy Links for the PopSet and list the organisms covered.

Access the Taxonomy record for *Mammuthus primigenius*. What is the origin of the mammoth’s specimens for some of the sequences reported in the Entrez databases? What is the lineage for mammoth? Which are the three major divisions of cellular organisms? Which of these has the highest number of entries in the “Structure” database?

II. OMIM, UniGene and Homologene

Perform an unlimited search for cytochrome c oxidase in the OMIM database. Repeat the query for “cytochrome c oxidase” as a term. Which search is more restrictive? Limit the retrieved entries only to those with gene location on chromosomes 4, 6 and 19. How many records have you retrieved? What is the chromosomal location of gene COX7A1 (OMIM record 123995)? Note the information about muscle and liver isoforms. Are there any known disease phenotypes (allelic variants) associated with the COX7A1 gene? Access the UniGene links from this record. Examine the expression profiles of the two genes. What do you conclude from the expression profiles? Access the Preview/Index page. Search for the UniGene records that have expression evidence of at least 100 ESTs? How many of these UniGene records are from mammals? Sort the records by organism.

Access the HomoloGene database and perform a search for records relating to COX genes (Preview/Index—gene name and use *cox** as a query). How many records do you retrieve? Are COX7A1 and COX7A2 members of the same HomoloGene group? Are all COX genes equally conserved in evolution? What are their common ancestors? Are there any COX genes that are conserved throughout the superkingdom of Eukaryota (Use the Preview/Index page—ancestor-- (*Taxonomy ID: 2759*)? Display the taxonomy tree for organisms included in the HomoloGene COX1 record.

III. dbSNP

Access the SNP database and select its Limits page. Check the appropriate boxes to allow selection for human nonsynonymous SNPs in the coding regions of chromosome 22. Add two more requirements that the SNP has an OMIM link and is associated with a structure. Retrieve and download the UI List for these records. Use the saved file to retrieve the records with the UI List in Batch Entrez.

The screenshot shows the NCBI homepage. A red rectangle highlights the search bar area, which includes a dropdown menu set to 'All Databases' and a text input field containing 'mammoth'. A red arrow points to the 'Search' button next to the input field. The page layout includes a left sidebar with 'Resources' (NCBI Home, All Resources (A-Z), Literature, DNA & RNA, Proteins, Sequence Analysis, Genes & Expression, Genomes & Maps, Domains & Structures, Genetics & Medicine, Taxonomy, Data & Software, Training & Tutorials, Homology, Small Molecules, Variation), a central 'Welcome to NCBI' section with a 'Genome Reference Consortium' banner and a 'How To...' list, and a right sidebar with 'Popular Resources' (PubMed, PubMed Central, Bookshelf, BLAST, Gene, Nucleotide, Protein, GEO, Conserved Domains, Structure, PubChem) and 'NCBI News' (March News issue, NIH announces Genetic Testing Registry, BLAST+ in print).

NCBI Entrez, The Life Sciences Search Engine

HOME SEARCH SITE MAP PubMed All Databases Human Genome GenBank Map Viewer

Search across databases mammoth GO Clear Help

- Result counts displayed in gray indicate one or more terms not found

337	PubMed: biomedical literature citations and abstracts	5	Books: online books
1018	PubMed Central: free, full text journal articles	2	OMIM: online Mendelian Inheritance in Man
5	Site Search: NCBI web and FTP sites	1	OMIA: online Mendelian Inheritance in Animals
65716	Nucleotide: Core subset of nucleotide sequence records	none	dbGaP: genotype and phenotype
none	EST: Expressed Sequence Tag records	2	UniGene: gene-oriented clusters of transcript sequences
none	GSS: Genome Survey Sequence records	none	CDD: conserved protein domain database
626	Protein: sequence database	none	3D Domains: domains from Entrez Structure
2	Genome: whole genome sequences	none	UniSTS: markers and mapping data
none	Structure: three-dimensional macromolecular structures	48	PopSet: population study data sets
2	Taxonomy: organisms in GenBank	none	GEO Profiles: expression and molecular abundance profiles
none	SNP: single nucleotide polymorphism	1	GEO DataSets: experimental sets of GEO data
none	dbVar: Genomic structural variation	none	Cancer Chromosomes: cytogenetic databases

NCBI Resources How To

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Search: PubMed mammoth Search Clear

RSS Save search Limits Advanced search Help

Display Settings: Summary, 200 per page, Sorted by Recently Added

Results: 1 to 200 of 337

<< First < Prev Page

- ☐ [Lipids and the ocular lens.](#)
- 1. Borchman D, Yappert MC.
J Lipid Res. 2010 Apr 20. [Epub ahead of print]
PMID: 20407021 [PubMed - as supplied by publisher]
- ☐ [Temporal genetic change in the last remaining population of woolly mammoth.](#)
- 2. Nyström V, Dalén L, Vartanyan S, Lidén K, Ryman N, Angerbjörn A.
Proc Biol Sci. 2010 Mar 31. [Epub ahead of print]
PMID: 20356891 [PubMed - as supplied by publisher]
[Related citations](#)
- ☐ [Large-scale prediction of protein-protein interactions from structures.](#)
- 3. Hue M, Riffle M, Vert JP, Noble WS.
BMC Bioinformatics. 2010 Mar 18;11:144.
PMID: 20298601 [PubMed - in process] [Free PMC Article](#) [Free text](#)
[Related citations](#)

☐ [Evolution: memories of mammoths.](#)

112. Gee H.
Nature. 2006 Feb 9;439(7077):673. No abstract available.
PMID: 16467828 [PubMed - indexed for MEDLINE]
[Related citations](#)

☐ [Complete mitochondrial genome and phylogeny of Pleistocene mammoth *Mammuthus primigenius*.](#)

113. Rogaev EI, Moliaka YK, Malyarchuk BA, Kondrashov FA, Derenko MV, Chumakov I, Grigorenko AP.
PLoS Biol. 2006 Mar;4(3):e73. Epub 2006 Feb 7.
PMID: 16448217 [PubMed - indexed for MEDLINE] [Free PMC Article](#) [Free text](#)
[Related citations](#)

☐ [The year of the mammoth.](#)

114. Cooper A.
PLoS Biol. 2006 Mar;4(3):e78. Epub 2006 Feb 7. No abstract available.
PMID: 16448215 [PubMed - indexed for MEDLINE] [Free PMC Article](#) [Free text](#)
[Related citations](#)

☐ [The role of zoos in the rehabilitation of animals in the circus.](#)

115. Gupta BK, Chakraborty B.
J Appl Anim Welf Sci. 2005;8(4):285-94.
PMID: 16436032 [PubMed - indexed for MEDLINE]
[Related citations](#)

NCBI Resources How To

PubMed
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Search: PubMed
mammoth[title]

RSS Save search Limits Advanced search Help

Search Clear

Display Settings: Summary, 200 per page, Sorted by Recently Added

Results: 143

☐ [Temporal genetic change in the last remaining population of woolly mammoth.](#)

1. Nyström V, Dalén L, Vartanyan S, Lidén K, Ryman N, Angerbjörn A.
Proc Biol Sci. 2010 Mar 31. [Epub ahead of print]
PMID: 20356891 [PubMed - as supplied by publisher]
[Related citations](#)

☐ [Scientific cooperation. African physicists set their sights on mammoth scope.](#)

2. Bohannon J.
Science. 2010 Jan 22;327(5964):400. No abstract available.
PMID: 20093443 [PubMed]
[Related citations](#)

☐ [Complete mitochondrial genome and phylogeny of Pleistocene mammoth *Mammuthus primigenius*.](#)

37. Rogaev EI, Moliaka YK, Malyarchuk BA, Kondrashov FA, Derenko MV, Chumakov I, Grigorenko AP. PLoS Biol. 2006 Mar;4(3):e73. Epub 2006 Feb 7. PMID: 16448217 [PubMed - indexed for MEDLINE] [Free PMC Article](#) [Free text](#) [Related citations](#)

☐ [The year of the mammoth.](#)

38. Cooper A. PLoS Biol. 2006 Mar;4(3):e78. Epub 2006 Feb 7. No abstract available. PMID: 16448215 [PubMed - indexed for MEDLINE] [Free PMC Article](#) [Free text](#) [Related citations](#)

☐ [Ancient DNA. New methods yield mammoth samples.](#)

39. Gibbons A. Science. 2005 Dec 23;310(5756):1889. No abstract available. PMID: 16373545 [PubMed - indexed for MEDLINE] [Free Article](#) [Related citations](#)

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PLoS Biol. 2006 Mar;4(3):e78. Epub 2006 Feb 7.

The year of the mammoth.

Cooper A.
Australian Centre for Ancient DNA, Earth and Environmental Sciences, University of Adelaide, Adelaide, Australia. Alan.cooper@adelaide.edu.au
PMID: 16448215 [PubMed - indexed for MEDLINE] PMID: PMC1360097 [Free PMC Article](#)

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Results: 15

☐ Complete mitochondrial genome and phylogeny of Pleistocene mammoth *Mammuthus primigenius*.
1. Rogaev EI, Mollaka YK, Malyarchuk BA, Kondrashov FA, Derenko MV, Chumakov I, Grigorenko AP.
PLoS Biol. 2006 Mar;4(3):e73. Epub 2006 Feb 7.
PMID: 16448217 [PubMed - indexed for MEDLINE] Free PMC Article Free text
Related citations

☐ Genome sequencing in microfabricated high-density picolitre reactors.
2. Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM.
Nature. 2005 Sep 15;437(7057):376-80. Epub 2005 Jul 31. Erratum in: Nature. 2006 May 4;441(7089):120. Ho, Chun He [corrected to Ho, Chun Heen].
PMID: 16056220 [PubMed - indexed for MEDLINE] Free PMC Article Free text
Related citations

☐ Genomic sequencing of Pleistocene cave bears.
3. Noonan JP, Hofreiter M, Smith D, Priest JR, Rohland N, Rabeder G, Krause J, Dettler JC, Pääbo S, Rubin EM.
Science. 2005 Jul 22;309(5734):597-9. Epub 2005 Jun 2.
PMID: 15933159 [PubMed - indexed for MEDLINE] Free Article
Related citations

☐ Genetic analyses from ancient DNA.
4. Pääbo S, Poinar H, Serre D, Jaenicke-Despres V, Hebler J, Rohland N, Kuch M, Krause J, Vigilant L, Hofreiter M.
Annu Rev Genet. 2004;38:645-79. Review.
PMID: 15568989 [PubMed - indexed for MEDLINE]
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Q "Rothberg JM"[Author] (63)
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Q "Rogaev EI"[Author] (90)
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Nature. 2005 Sep 15;437(7057):376-80. Epub 2005 Jul 31.

Genome sequencing in microfabricated high-density picolitre reactors.

Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM.
454 Life Sciences Corp., 20 Commercial Street, Branford, Connecticut 06405, USA.
Erratum in:
Nature. 2006 May 4;441(7089):120. Ho, Chun He [corrected to Ho, Chun Heen].
Comment in:
Nature. 2005 Sep 15;437(7057):326-7.

Abstract
The proliferation of large-scale DNA-sequencing projects in recent years has driven a search for alternative methods to reduce time and cost. Here we describe a scalable, highly parallel sequencing system with raw throughput significantly greater than that of state-of-the-art capillary electrophoresis instruments. The apparatus uses a novel fibre-optic slide of individual wells and is able to sequence 25 million bases, at 99% or better accuracy, in one four-hour run. To achieve an approximately 100-fold increase in throughput over current Sanger sequencing technology, we have developed an emulsion method for DNA amplification and an instrument for sequencing by synthesis using a pyrosequencing protocol optimized for solid support and picolitre-scale volumes. Here we show the utility, throughput, accuracy and robustness of this system by shotgun sequencing and de novo assembly of the *Mycoplasma genitalium* genome with 96% coverage at 99.96% accuracy in one run of the machine.

PMID: 16056220 [PubMed - indexed for MEDLINE] PMCID: PMC1464427 Free PMC Article

Publication Types, MeSH Terms, Substances, Grant Support

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Related articles
Genomics: massively parallel sequencing. [Nature. 2005]
The complete genome of an individual by massively parallel DNA sequencing [Nature. 2008]
Assessing the feasibility of GS FLX Pyrosequencing for sequ [BMC Genomics. 2008]
Review The use of capillary electrophoresis for DNA polymorphism analysis [Mol Biotechnol. 2003]
Review Microfluidic devices for DNA sequencing: sample [Curr Opin Biotechnol. 2003]
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Cited by over 100 PubMed Central articles
De novo assembly of a 40 Mb eukaryotic genome from short sequence [PLoS Genet. 2010]
Comparative analysis of fecal microbiota in infants with and without eczema [PLoS One. 2010]
Exon-primed intron-crossing (EPIC) markers for non-model teleost fishes. [BMC Evol Biol. 2010]
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"Rothberg JM"[Author] Search Clear

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Results: 1 to 20 of 63

1. [Droplet microfluidic technology for single-cell high-throughput screening.](#)
Brouzes E, Medkova M, Savenelli N, Marran D, Twardowski M, Hutchison JB, Rothberg JM, Link DR, Perrimon N, Samuels ML.
Proc Natl Acad Sci U S A. 2009 Aug 25;106(34):14195-200. Epub 2009 Jul 15.
PMID: 19617544 [PubMed - indexed for MEDLINE] [Free PMC Article](#) [Free text](#)
[Related citations](#)
2. [High-throughput quantitative polymerase chain reaction in picoliter droplets.](#)
Kiss MM, Ortoleva-Donnelly L, Beer NR, Warner J, Bailey CG, Colston BW, Rothberg JM, Link DR, Leamon JH.
Anal Chem. 2008 Dec 1;80(23):8975-81.
PMID: 19551929 [PubMed - indexed for MEDLINE] [Free PMC Article](#) [Free text](#)
[Related citations](#)
3. [Low-abundance drug-resistant viral variants in chronically HIV-infected, antiretroviral treatment-naive patients significantly impact treatment outcomes.](#)
Simen BB, Simons JF, Hullsiek KH, Novak RM, Macarthur RD, Baxter JD, Huang C, Lubesi C, Turenchalk GS, Braverman MS, Desany B, Rothberg JM, Egholm M, Kozal MJ, Terry Beirn Community Programs for Clinical Research on AIDS.
J Infect Dis. 2009 Mar 1;199(5):693-701.
PMID: 19210162 [PubMed - indexed for MEDLINE]
[Related citations](#)
4. [The development and impact of 454 sequencing.](#)
Rothberg JM, Leamon JH.
Nat Biotechnol. 2008 Oct;26(10):1117-24.
PMID: 18846085 [PubMed - indexed for MEDLINE]
[Related citations](#)
5. [A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing.](#)
Green RE, Malaspina AS, Krause J, Briggs AW, Johnson PL, Uhler C, Meyer M, Good JM, Maricic T, Stenzel U, Prüfer K, Siebauer M, Burbano HA, Ronan M, Rothberg JM, Egholm M, Rudan P, Brajković D, Kučan Z, Gusic I, Wikström M, Laakkonen L, Kelso J, Slatkin M, Pääbo S.
Cell. 2008 Aug 8;134(3):416-26.
PMID: 18692465 [PubMed - indexed for MEDLINE] [Free PMC Article](#) [Free text](#)
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Search History

Search	Most Recent Queries	Time	Result
#14	Search "Rothberg JM"[Author]	13:49:13	63
#10	References for PMC Articles for PubMed (Select 16448215)	13:43:25	15
#12	Search "Rogaev EI"[Author]	13:24:11	90
#9	Related Citations for PubMed (Select 16448215)	13:23:15	105
#7	Search mammoth[title]	13:18:42	143
#6	Search mammoth	13:15:56	337

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Results: 1 to 20 of 337

- ☐ [Lipids and the ocular lens.](#)
1. Borchman D, Yappert MC.
J Lipid Res. 2010 Apr 20. [Epub ahead of print]
PMID: 20407021 [PubMed - as supplied by publisher]
- ☐ [Temporal genetic change in the last remaining population of woolly mammoth.](#)
2. Nyström V, Dalén L, Vartanyan S, Lidén K, Ryman N, Angerbjörn A.
Proc Biol Sci. 2010 Mar 31. [Epub ahead of print]
PMID: 20356891 [PubMed - as supplied by publisher]
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- ☐ [Large-scale prediction of protein-protein interactions from structures.](#)
3. Hue M, Riffle M, Vert JP, Noble WS.
BMC Bioinformatics. 2010 Mar 18;11:144.
PMID: 20298601 [PubMed - in process] [Free PMC Article](#) [Free text](#)
[Related citations](#)
- ☐ [Lost giants.](#)
4. Choi CQ.
Sci Am. 2010 Feb;302(2):21-2. No abstract available.
PMID: 20128214 [PubMed - indexed for MEDLINE]
[Related citations](#)
- ☐ [Multiple structure alignment and consensus identification for proteins.](#)
5. Iljinkin I, Ye J, Janardan R.

Find related data Database: PopSet Sets of sequences from population and evolutionary genetic studies in the PopSet database reported in the current articles. Find items

Search details Turn Off "mammoth" [MeSH Terms] OR "mammoth" [All Fields] OR "mammoth" [All Fields] Search See more...

NCBI PopSet

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search: PopSet for Go Clear

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Items 1 - 18 of 18 One page.

- ☐ [Out of America: ancient DNA evidence for a new world origin of late quaternary woolly mammoths.](#)
1. GI:198241407
- ☐ [Global phylogeny of lions](#)
2. GI:114384091
- ☐ [Global phylogeny of lions](#)
3. GI:114384067
- ☐ [Ancient DNA forces reconsideration of evolutionary history of Mediterranean pygmy elephants.](#)
4. GI:84784058
- ☐ [A nuclear DNA phylogeny of the woolly mammoth \(Mammuthus primigenius\).](#)
5. GI:82569635

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- mammoth (337)
- "Rothberg JM" [Author] (63)
- Genome sequencing in microfabricated high-density picolitre reactors.
- "Rogaev EI" [Author] (90) PubMed
- Complete mitochondrial genome and phylogeny of Pleistocene mammoth Mammuthus primigenius.

See more...

- ☐ [Diverse plant and animal genetic records from Holocene and Pleistocene sediments.](#)
16. GI:32396546
- ☐ [Evolution of endogenous retrovirus-like elements of the woolly mammoth \(Mammuthus primigenius\) and its relatives.](#)
17. GI:14090839
- ☐ [Evolution of endogenous retrovirus-like elements of the woolly mammoth \(Mammuthus primigenius\) and its relatives.](#)
18. GI:13898381

Items 1 - 18 of 18 One page.

NCBI PopSet

Search PopSet for [] Go Clear

Display PopSet Show 1 Send to []

1: [Greenwood AD](#). Reports Evolution of endo...[gi:14090839] [Links](#)

Evolution of endogenous retrovirus-like elements of the woolly mammoth (*Mammuthus primigenius*) and its relatives.

Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
View citation in [PubMed](#)

Generate an alignment using BLAST with these options

Blast Options Word Size: 20 Expect Value: 1e-06 Master Sequence: AF312038.1

Display Options ☒ Show only highest scoring alignments ☐ Show all generated alignments

[Generate Alignment](#)

1	AF312038.1	CCTACCTCAG	AGCTACATCA	ACTCTCCAGC	CCTATGTCAT	AATTTTGTTC	TAGAGGGAAC	(1-60)
2	AF312039.1	CCTACCTCAG	CGCTACATTA	GCTCTCCAGC	CCTATGTCAT	AATTTAGT-C	CACAGTGGTT	(1-59)
3	AF312040.1	CCTACCTCAG	AGTTACATCA	ACTCTCCAGC	CCTATATCAT	AATTTAGT-C	CAGAGGGAAC	(1-59)
4	AF312041.1	CCTGCTCAG	AATACATCA	ACTCTCCAGC	CGTATGTCAT	AATTTAGT-C	TGCAGGAATC	(1-59)
5	AF312042.1	CCTACCTCAG	AGTTACATCA	ACTCTCCAGC	CCTATATCAT	AATTTAGT-C	CAGAGGGAAC	(1-59)
6	AF312043.1	TTTACCTGAG	GGATACATCA	ACTCTCCAGC	TCTATGTCAT	AATTTAGT-C	CTCAGGGAAC	(1-59)

NCBI PopSet

Search PopSet for [] Go Clear

Display PopSet Show 1 Send to []

1: [Greenwood AD](#). Reports Evolution of endo...[gi:14090839] [Links](#)

Evolution of endogenous retrovirus-like elements of the woolly mammoth (*Mammuthus primigenius*) and its relatives.

Greenwood,A.D., Lee,F., Capelli,C., DeSalle,R., Tikhonov,A., Marx,P.A., MacPhee,R.D.
Mol. Biol. Evol. 18 (5), 840-847 (5 2001)
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- Nucleotide
- PubMed
- Taxonomy
- Taxonomy Tree

NCBI Nucleotide

Search Nucleotide for

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Display Summary Show 20 Sort By Send to

All: 170 Bacteria: 0 INSDC (GenBank): 170 RefSeq: 0 mRNA: 0

Items 1 - 20 of 170

1. [Procavia capensis clone Pc10 endogenous retrovirus ERV-L pol gene, partial sequence](#)
109 bp linear genomic
AF312207.1 GI:14091008

2. [Procavia capensis clone Pc9 endogenous retrovirus ERV-L pol gene, partial sequence](#)
83 bp linear genomic
AF312206.1 GI:14091007

3. [Procavia capensis clone Pc8 endogenous retrovirus ERV-L pol gene, partial sequence](#)
83 bp linear genomic
AF312205.1 GI:14091006

4. [Procavia capensis clone Pc7 endogenous retrovirus ERV-L pol gene, partial sequence](#)
83 bp linear genomic
AF312204.1 GI:14091005

5. [Procavia capensis clone Pc6 endogenous retrovirus ERV-L pol gene, partial sequence](#)
109 bp linear genomic
AF312203.1 GI:14091004

6. [Procavia capensis clone Pc5 endogenous retrovirus ERV-L pol gene, partial sequence](#)
109 bp linear genomic
AF312202.1 GI:14091003

Top Organisms [Tree]

- Mammuthus primigenius (90)
- Loxodonta africana (30)
- Elephas maximus (30)
- Procavia capensis (10)
- Trichechus manatus (10)

Recent activity

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- Nucleotide Links for PopS... (170) Nucleotide
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NCBI Taxonomy

Search Taxonomy for

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1. [Mammuthus primigenius](#) (woolly mammoth), species, mammals

2. [Procavia capensis](#) (cape rock hyrax), species, mammals

3. [Loxodonta africana](#) (African savanna elephant), species, mammals

4. [Elephas maximus](#) (Asiatic elephant), species, mammals

5. [Trichechus manatus](#) (Caribbean manatee), species, mammals

One page.

Links

Links

Links

Links

Links

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name ☐ lock

Display levels using filter:

Mammuthus primigenius

Taxonomy ID: 37349

Genbank common name: woolly mammoth
 Inherited blast name: placentals
 Rank: species
 Genetic code: [Translation table 1 \(Standard\)](#)
 Mitochondrial genetic code: [Translation table 2 \(Vertebrate Mitochondrial\)](#)
 Other names:
 common name: mammoth

[Lineage\(full \)](#)
[cellular organisms](#); [Eukaryota](#); [Fungi/Metazoa group](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Coelomata](#);
[Deuterostomia](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#);
[Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Afrotheria](#); [Proboscidea](#); [Elephantidae](#); [Mammuthus](#)

Entrez records	
Database name	Direct links
Nucleotide	284
Protein	422
Genome Sequences	1
Genome Projects	3
Popset	10
PubMed Central	38
Gene	13
SRA Experiments	22
Taxonomy	1

Comments and References:

extinct
 This taxon is extinct.

Genome Information

[Go to NCBI genomic BLAST page for Mammuthus primigenius](#)

Trace records (raw single-pass reads of DNA sequence)	
Sequencing Center Name	
Record counts per type	
454	ALL
CCGB - Center for Comparative Genomics and Bioinformatics, PennState University, USA	
303,789	303,789
Totals per type	
303,789	303,789

External Information Resources (NCBI LinkOut)



LinkOut	Subject	LinkOut Provider
Mammuthus primigenius taxonomy	taxonomy/phylogenetic	Arctos Specimen Database

Notes:
 Groups interested in participating in the LinkOut program should visit the [LinkOut home page](#).
 A list of our current non-bibliographic LinkOut providers can be found [here](#).
 To see LinkOut links in this lineage click [here](#)

Information from sequence entries

[Show organism modifiers](#)

Organism modifiers			
To hide organism modifiers click here			
isolate			
2000/173 [3 1 3]	2000/174 [1 1 1]	2000/183 [1 1 1]	2000/198 [1 1 1]
2000/78 [1 1 1]	2001/412 [1 1 1]	2001/413 [1 1 1]	2002/472 [3 1 3]
2002/473 [2 2]	2002/594 [1 1 1]	2005/898 [1 1 1]	2005/915 [2 2]
2005/917 [2 2]	2005/928 [1 1 1]	2005/930 [1 1 1]	2005/988 [1 1 1]
2005/999 [1 1 1]	2006/001 [1 1 1]	33,000 year-old woolly mammoth [1 1]	AK-323-V-I [1 1 1]
AM 4136 [1 1]	AM 493 [1 1]	AM 8744 [1 1]	AM104 [1 1 1]
AM1131 [1 1 1]	AM1187 [1 1 1]	AM1189 [1 1 1]	AM1193 [1 1 1]
AM1208 [1 1 1]	BL-O13 [1 1]	BL-O179 [1 1]	BL-O208 [1 1]
BL-O219 [1 1]	BL-O240 [1 1]	BL-O250 [1 1]	BL-O308 [1 1]
BL-O309 [1 1]	BL-O310 [1 1]	BL-O443 [1 1]	BL-O503 [1 1]
BL-O585 [1 1]	BL-O59 [1 1]	BL-O723 [1 1]	BL-O865 [1 1]
BR.10 [1 1]	Ber10 [1 1 1]	Ber11 [1 1 1]	Ber12 [2 2]
Ber16 [1 1 1]	Ber20 [1 1 1]	Ber28 [1 1 1]	Ber5 [1 1 1]
Ber9 [1 1 1]	Chekurovka [1 1]	Eng.Creek.A [2 2 1]	Eng.Creek.A3 [1 1]
Eng.Creek.A5 [1 1]	Eng.Creek.B [2 2 1]	Eng.Creek.B3 [1 1]	Eng.Creek.B5 [1 1]
Engineer Creek [1 1]	GDY1 [1 1 1]	IK-01-359 [1 1 1]	IK-98-1087 [1 1 1]
IK-99-235 [1 1 1]	IK-99-322 [1 1 1]	IK-99-5001 [1 1 1]	IK-99-524 [1 1 1]
IK-99-70 [1 1 1]	ILC.01(10915) [1 1]	ILC.04(11028) [1 1]	ILC.06(1138a) [1 1]

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for as complete name ☒ lock

Display 3 levels using filter: none

Mammuthus primigenius

Taxonomy ID: 37349
Genbank common name: woolly mammoth
Inherited blast name: placentals
Rank: species
Genetic code: [Translation table 1 \(Standard\)](#)
Mitochondrial genetic code: [Translation table 2 \(Vertebrate Mitochondrial\)](#)
Other names:
common name: **mammoth**

Lineage (full)
[cellular organisms](#); [Eukaryota](#); [Fungi/Metazoa group](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Coelomata](#); [Deuterostomia](#); [Chordata](#); [Cranata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#); [Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Afrotheria](#); [Proboscidea](#); [Elephantidae](#); [Mammuthus](#)

Comments and References:
extinct
This taxon is extinct.

Entrez records	
Database name	Direct links
Nucleotide	284
Protein	422
Genome Sequences	1
Genome Projects	3
Popset	10
PubMed Central	38
Gene	13
SRA Experiments	22
Taxonomy	1

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for: as complete name ☒ lock Go Clear

Display: levels using filter: none

☐ Nucleotide ☐ Protein ☐ Structure ☐ Genome Sequences ☐ Genome Projects ☐ Popset ☐ SNP
☐ 3D Domains ☐ Domains ☐ GEO Datasets ☐ GEO Expressions ☐ UniGene ☐ UniSTS ☐ PubMed Central
☐ Gene ☐ HomoloGene ☐ MapView ☐ LinkOut ☐ BLAST ☐ TRACE

Lineage (full): [root](#)

◊ [cellular organisms](#) Click on organism name to get more information.

- ◊ [Archaea](#)
 - ◊ [Crenarchaeota](#) (eocytes)
 - [Thermoprotei](#)
 - [unclassified Crenarchaeota](#)
 - [environmental samples](#)
 - ◊ [Euryarchaeota](#)
 - [Archaeoglobi](#)
 - [Halobacteria](#)

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for: as complete name ☒ lock Go Clear

Display: levels using filter: none

☐ Nucleotide ☐ Nucleotide Core ☐ Nucleotide EST ☐ Nucleotide GSS ☐ Protein ☐ Structure ☐ Genome Sequences
☐ Genome Projects ☐ Popset ☐ SNP ☐ 3D Domains ☐ Domains ☐ GEO Datasets ☐ GEO Profiles
☐ UniGene ☐ UniSTS ☐ PubMed Central ☐ Gene ☐ HomoloGene ☐ MapView ☐ LinkOut
☐ BLAST ☐ TRACE ☐ Taxonomy

Lineage (full): [root](#)

◊ [cellular organisms](#) Click on organism name to get more information.

- ♦ [Archaea](#)
- ♦ [Bacteria](#) (eubacteria)
- ♦ [Eukaryota](#) (eucaryotes)

NCBI Taxonomy Browser

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy

Search for: as complete name ☒ lock Go Clear

Display: levels using filter: none

☐ Nucleotide ☐ Nucleotide EST ☐ Nucleotide GSS ☐ Protein ☒ Structure ☐ Genome Sequences ☐ Genome Projects
☐ Popset ☐ SNP ☐ 3D Domains ☐ Domains ☐ GEO Datasets ☐ GEO Expressions ☐ UniGene
☐ UniSTS ☐ PubMed Central ☐ Gene ☐ HomoloGene ☐ OMIA ☐ SRA Experiments ☐ MapView
☐ LinkOut ☐ BLAST ☐ TRACE

Lineage (full): [root](#)

◊ [cellular organisms](#) [57,960](#) Click on organism name to get more information.

- [Archaea](#) [2,605](#)
- [Bacteria](#) (eubacteria) [23,055](#)
- [Eukaryota](#) (eucaryotes) [32,681](#)

Example1, Part II

The screenshot shows the NCBI (National Center for Biotechnology Information) homepage. At the top, there is a navigation bar with 'NCBI', 'Resources', and 'How To' links. Below this, the NCBI logo and name are displayed. A search bar is prominently featured, containing the text 'cytochrome C oxidase'. The search bar is highlighted with a red rectangle, and a red arrow points to the 'Search' button. The search results are not yet displayed. The page layout includes a left sidebar with a 'Resources' menu, a central 'Welcome to NCBI' section with a 'PubMed Central' banner, and a right sidebar with 'Popular Resources' and 'NCBI News' sections.

NCBI Resources ▾ How To ▾

NCBI
National Center for
Biotechnology Information

Search OMIM ▾
cytochrome C oxidase **Search** Clear

Resources

- NCBI Home
- All Resources (A-Z)
- Literature
- DNA & RNA
- Proteins
- Sequence Analysis
- Genes & Expression
- Genomes & Maps
- Domains & Structures
- Genetics & Medicine
- Taxonomy
- Data & Software
- Training & Tutorials
- Homology
- Small Molecules
- Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

[More about the NCBI](#) | [Mission](#) | [Organization](#) | [Research](#) | [RSS](#)

PubMed Central

Free Full Text. Over 1,500,000 articles from over 450 journals. Linked to PubMed and fully searchable.

1 2 3 4

How To...

- Obtain the full text of an article
- Retrieve all sequences for an organism or taxon
- Find a homolog for a gene in another organism
- Find genes associated with a phenotype or disease
- Design PCR primers and check them for specificity
- Find the function of a gene or gene product
- Determine conserved synteny between the genomes of two organisms

[See all ...](#)

NLM/NCBI H1N1 Flu Resources

Popular Resources

- PubMed
- PubMed Central
- Bookshelf
- BLAST
- Gene
- Nucleotide
- Protein
- GEO
- Conserved Domains
- Structure
- PubChem

NCBI News

[March News issue available](#) 09 Apr 2010
Includes My NCBI, E-Utility, and BLAST news.

[NIH announces Genetic Testing Registry](#) 23 Mar 2010
NCBI will be responsible for developing the regist...

[BLAST+ in print](#) 19 Mar 2010
A newly published article describes improvements and new fea...

[More...](#)

NCBI OMIM Online Mendelian Inheritance in Man Johns Hopkins University

All Databases PubMed Nucleotide Protein Genome Structure PMC OMIM

Search OMIM for cytochrome C oxidase Go Clear Save Search

Limits Preview/Index History Clipboard Details

Display Titles Show 20 Send to

All: 130 OMIM UniSTS: 23 OMIM dbSNP: 28

Items 1 - 20 of 130 Page 1 of 7 Next

- ☐ 1: *516030
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1
GeneTests, Links
- ☐ 2: *516040
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT II; MTCO2
GeneTests, Links
- ☐ 3: *124089
CYTOCHROME c OXIDASE, SUBUNIT VIb, POLYPEPTIDE 1; COX6B1
Gene map locus [19q13.1](#)
MGI, GeneTests, Links
- ☐ 4: #604377
CARDIOENCEPHALOMYOPATHY, FATAL INFANTILE, DUE TO CYTOCHROME c OXIDASE DEFICIENCY
Gene map locus [22q13](#)
GeneTests, Links
- ☐ 5: *516050
CYTOCHROME c OXIDASE III; MTCO3
GeneTests, Links

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All Databases PubMed Nucleotide Protein Genome Structure PMC OMIM

Search OMIM for "cytochrome C oxidase" Go Clear Save Search

Limits Preview/Index History Clipboard Details

Display Titles Show 20 Send to

All: 103 OMIM UniSTS: 17 OMIM dbSNP: 13

Items 1 - 20 of 103 Page 1 of 6 Next

- ☐ 1: *516030
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1
GeneTests, Links
- ☐ 2: *516040
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT II; MTCO2
GeneTests, Links
- ☐ 3: *124089
CYTOCHROME c OXIDASE, SUBUNIT VIb, POLYPEPTIDE 1; COX6B1
Gene map locus [19q13.1](#)
MGI, GeneTests, Links
- ☐ 4: #604377
CARDIOENCEPHALOMYOPATHY, FATAL INFANTILE, DUE TO CYTOCHROME c OXIDASE DEFICIENCY
Gene map locus [22q13](#)
GeneTests, Links
- ☐ 5: *516050
CYTOCHROME c OXIDASE III; MTCO3
GeneTests, Links
- ☐ 6: *123864
CYTOCHROME c OXIDASE, SUBUNIT IV, ISOFORM 1; COX4I1
Gene map locus [16q22-qter](#)
MGI, Links

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Search OMIM for Go Clear

Limits Preview/Index History Clipboard Details

Display Detailed Show 20 Send to

***516030** GeneTests, Links

COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT I; MTCO1

Alternative titles; symbols

CYTOCHROME c OXIDASE I; CO1

TEXT

DESCRIPTION

Cytochrome c oxidase subunit I (CO1 or MTCO1) is 1 of 3 mitochondrial DNA (mtDNA) encoded subunits (MTCO1, MTCO2, MTCO3) of respiratory Complex IV. Complex IV is located within the mitochondrial inner membrane and is the third and final enzyme of the electron transport chain of mitochondrial oxidative phosphorylation. It collects electrons from reduced cytochrome c and transfers them to oxygen to give water. The energy released is used to transport protons across the mitochondrial inner membrane. Complex IV is composed of 13 polypeptides. Subunits I, II, and III (MTCO1, MTCO2, MTCO3) are encoded by mtDNA while subunits IV, Va, Vb, VIa, VIb, VIc, VIIa, VIIb, VIIc, and VIII are nuclear encoded (Kadenbach et al., 1983; Shoffner and Wallace, 1995). While the mammalian Complex IV has a complex structure, several prokaryotic enzyme systems have the same catalytic functions, but are much simpler. These systems have been amenable to cloning and in vitro imaging, thus permitting detailed structure-function studies. Two well-studied systems are the cytochrome aa3 (cytochrome c oxidase) of Rhodospirillum rubrum and the cytochrome bo (ubiquinol oxidase) of Escherichia coli. The R. rubrum enzyme has 3 subunits that are homologous to the 3 mammalian mtDNA subunits. R. rubrum subunit I is 62.1 kD and 52% identical and 76% similar to beef heart MTCO1; subunit II is 32.9 kD and 39% identical and 63% similar to beef MTCO2, and subunit III is 30.1 kD and 49% identical and 71% similar to beef heart. The Soret max = 444.5 nm (bovine = 443 nm) and alpha-band max = 606 nm (bovine = 604 nm). The extinction coefficients are identical (Hosler et al., 1993). These and other studies (Capaldi, 1990) have generated the following functional outlines for this enzyme. [30 PubMed Neighbors](#)

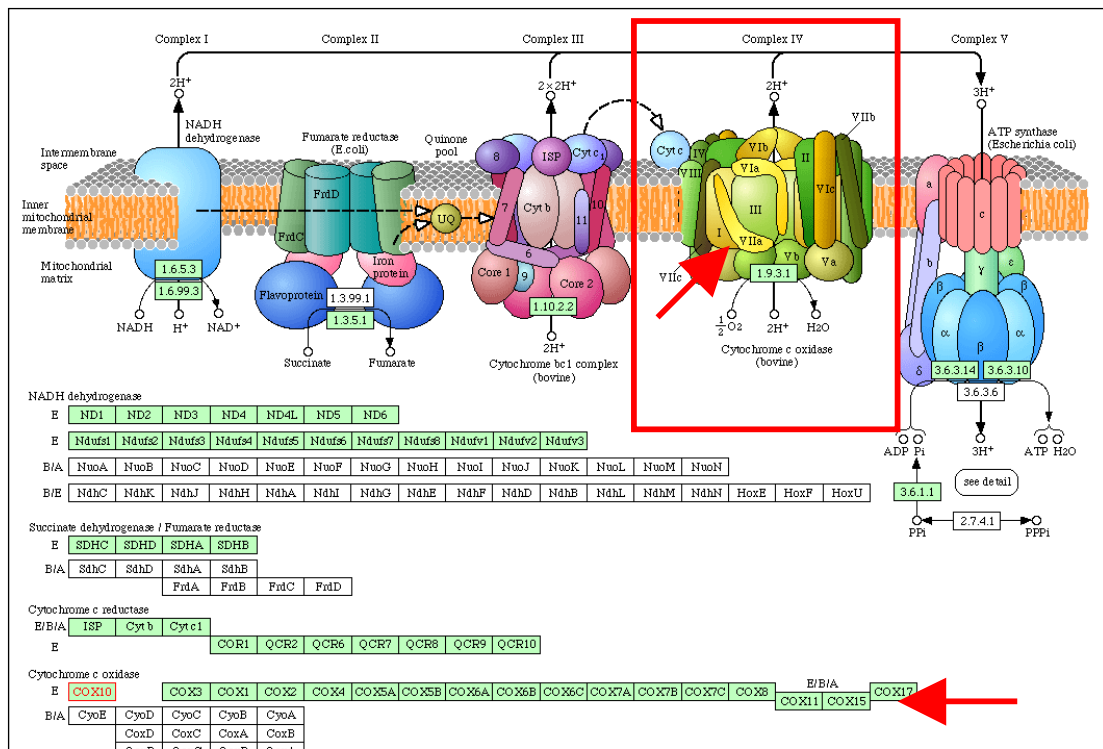


Figure from KEGG **Oxidative phosphorylation - Reference pathway (KO)**
http://www.genome.jp/dbget-bin/show_pathway?hsa00190+4512

Entrez

OMIM
Search OMIM
Search Gene Map
Search Morbid Map

Help
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How to Link

FAQ
Numbering System
Symbols
How to Print
Citing OMIM
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OMIM Facts
Statistics
Update Log
Restrictions on Use

Allied Resources
Genetic Alliance
Databases
HGMD
Leaves Specific

Limits
Preview/Index
History
Clipboard
Details

- To Search all fields, leave the following boxes unchecked.
- To narrow the search, check the boxes with specific fields' names, or use [search field tags](#) enclosed in square brackets, e.g. `aaa[title]`.
- [Boolean operators](#) AND, OR, NOT must be in upper case.

Search in Field(s):
clear

☐ Title
☐ MIM number
☐ Allelic Variants

☐ Text
☐ References
☐ Clinical Synopsis

☐ Gene Map Disorder
☐ Contributors

Chromosome(s):
clear

☐ 1
☐ 2
☐ 3
☒ 4
☐ 5
☒ 6
☐ 7
☐ 8

☐ 9
☐ 10
☐ 11
☐ 12
☐ 13
☐ 14
☐ 15
☐ 16

☐ 17
☐ 18
☒ 19
☐ 20
☐ 21
☐ 22
☐ X
☐ Y

☐ mitochondrial
☐ unknown

MIM Number Prefix:
clear

☐ * gene with known sequence

☐ + gene with known sequence and phenotype

☐ # phenotype description, molecular basis known

☐ % mendelian phenotype or locus, molecular basis unknown

☐ none other, mainly phenotypes with suspected mendelian basis

Only Records with:
clear

☐ Allelic Variants

☐ Clinical Synopsis

☐ Gene map locus

NCBI

OMIM
Online Mendelian Inheritance in Man

Johns Hopkins University

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Nucleotide
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Genome
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Search OMIM for "cytochrome C oxidase" Go Clear Save Search

Limits
Preview/Index
History
Clipboard
Details

Limits: chromosome 4, chromosome 6, chromosome 19

Display Titles Show 20 Send to

All: 15 OMIM UniSTS: 4 OMIM dbSNP: 4

Items 1 - 15 of 15 One page.

☐ 1: *124089
CYTOCHROME c OXIDASE, SUBUNIT VIb, POLYPEPTIDE 1; COX6B1
Gene map locus [19q13.1](#)

☐ 2: *123995
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 1; COX7A1
Gene map locus [19q13.12](#)

☐ 3: *123996
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 2; COX7A2
Gene map locus [6q12](#)

☐ 4: *123997
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 3; COX7A3
Gene map locus [4q22](#)

☐ 5: #220110
MITOCHONDRIAL COMPLEX IV DEFICIENCY
Gene map locus [2q33.3, 19q13.1](#)

☐ 6: *609811
CYTOCHROME C OXIDASE SUBUNIT VIIb2; COX7B2

☐ 7: #256000
LEIGH SYNDROME; LS
LEIGH SYNDROME DUE TO MITOCHONDRIAL COMPLEX I DEFICIENCY, INCLUDED
Gene map locus [11q13, 11q13, 11p11.1, 10q24, 9q34, 8q22.1, 7q31-q32, 5q31.2, 5q11.1, 5p15, 2q33, 19p13](#)

***123995**
CYTOCHROME c OXIDASE, SUBUNIT VIIa, POLYPEPTIDE 1; COX7A1

Alternative titles; symbols
CYTOCHROME c OXIDASE, SUBUNIT VIIa, MUSCLE ISOFORM; COX7AM

Gene map locus [19q13.12](#)

TEXT

DESCRIPTION

Cytochrome c oxidase (COX; [EC 1.9.3.1](#)), the last component of the mitochondrial respiratory chain, catalyzes the transfer of electrons from reduced molecular oxygen. In mammals, the apoprotein is composed of 3 large catalytic subunits, encoded by the mitochondrial genome ([516030](#), [516040](#)), smaller, nuclear-encoded subunits which may play a regulatory role. Subunit VIIa of mammalian COX exists in at least 2 isoforms, liver (see [123995](#)) and muscle (see [123996](#)). [PubMed Neighbors](#)

CLONING

[Araudo et al. \(1992\)](#) isolated a full-length cDNA encoding the COX7A muscle isoform. The deduced polypeptide shares 78% identity with the bovine muscle form but only 63% identity with the human liver isoform. Northern blot analysis of primate tissues demonstrated that mRNA for the muscle form is present only in muscle tissues; in contrast, liver mRNA is present in both muscle and nonmuscle tissues. [30 PubMed Neighbors](#)

[Fabrizi et al. \(1989\)](#) reported the sequence of the human COX7A1 gene.

Links

- ▶ BioSystems
- ▶ Gene
- ▶ GEO Profiles
- ▶ HomoloGene
- ▶ Map Viewer
- ▶ Free in PMC
- ▶ PubMed (calculated)
- ▶ PubMed (cited)
- ▶ Gene Genotype
- ▶ GeneView in dbSNP
- ▶ UniGene
- ▶ Related Entries
- ▶ Nucleotide
- ▶ Protein
- ▶ LinkOut

NCBI **UniGene**
 ORGANIZED VIEW OF THE TRANSCRIPTOME

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals

Search UniGene for Go Clear

Limits Preview/Index History Clipboard Details


Display Summary Show 20 Sort By Send to

All: 2 Fungi: 0 Insects: 0 Mammals: 2 Plants: 0

Items 1 - 2 of 2 One page.

☐ **1:** [Cytochrome c oxidase subunit VIIa polypeptide 1 \(muscle\)](#)
 COX7A1, *Homo sapiens*
 Hs.421621: 264 sequences.
[Order cDNA clone](#)

☐ **2:** [Cytochrome c oxidase subunit VIIa polypeptide 2 \(liver\)](#)
 COX7A2, *Homo sapiens*
 Hs.70312: 726 sequences.
[Order cDNA clone](#)


UniGene
ORGANIZED VIEW OF THE TRANSCRIPTOME

Nucleotide
Protein
Genome
Structure
Popset
Taxonomy

Go Clear

UGID:224558 UniGene Hs.421621 Homo sapiens (human) COX7A1

Order cDNA clone, Links

Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1)

SELECTED PROTEIN SIMILARITIES

Comparison of sequences in UniGene with selected protein reference sequences. The alignments can suggest function of a gene.

	Reference Protein	Species	Id(%)	Len(aa)
NP_001855.1	cytochrome c oxidase subunit 7A1, mitochondrial precursor	<i>H. sapiens</i>	100.0	78
NP_034074.1	cytochrome c oxidase subunit 7A1, mitochondrial precursor	<i>M. musculus</i>	74.7	79

GENE EXPRESSION

Tissues and development stages from this gene's sequences survey gene expression. Links to other NCBI expression resources.

EST Profile: Approximate expression patterns inferred from EST sources.
[\[Show more entries with profiles like this\]](#)

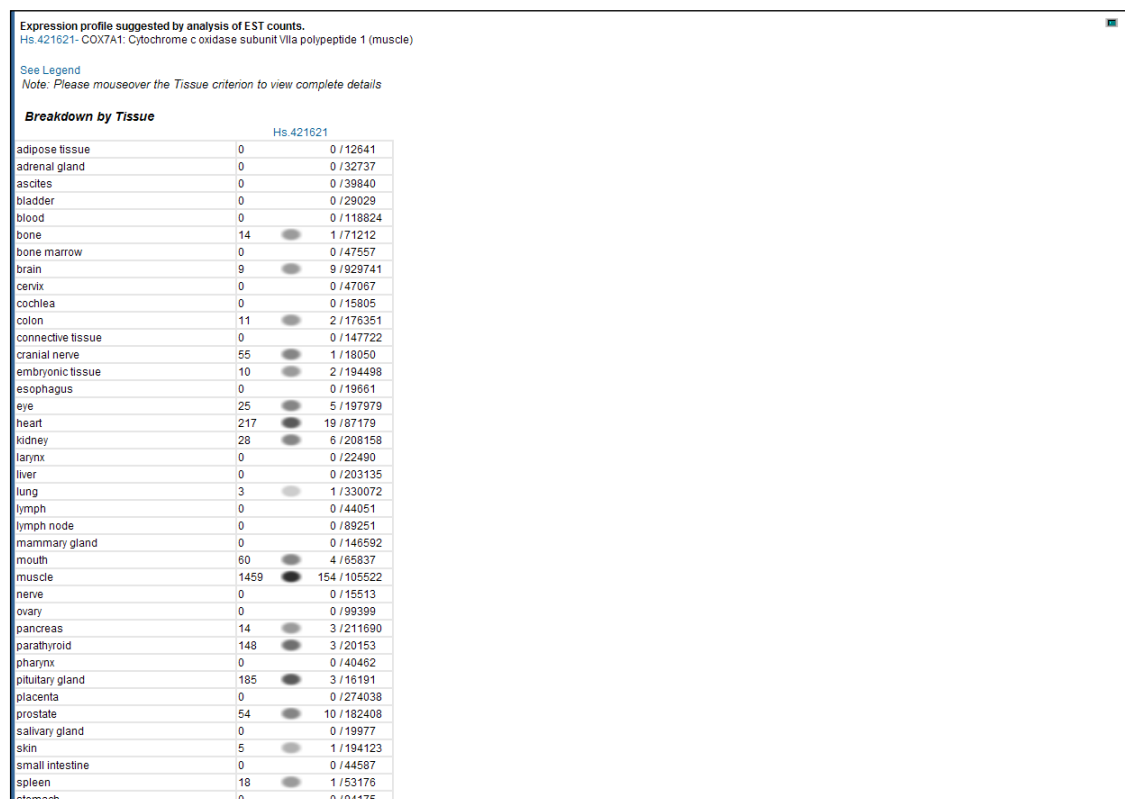
GEO profiles: Experimental gene expression data (Gene Expression Omnibus).

cDNA Sources: muscle; heart; mixed; prostate; brain; embryonic tissue; uncharacterized tissue; pancreas; parathyroid; lung; thyroid; vascular; spleen; eye; kidney; intestine; mouth; pituitary gland; uterus; umbilical cord; skin; bone

MAPPING POSITION

Genomic location specified by transcript mapping, radiation hybrid mapping, genetic mapping or cytogenetic mapping.

Chromosome: 19
Map position: 19q13.1
UniSTS entry: Chr 19 [RH93348](#)



NCBI  **UniGene**
ORGANIZED VIEW OF THE TRANSCRIPTOME

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Search UniGene for Go Clear

Limits **Preview/Index** History Clipboard Details


Display Summary Show 20 Sort By Send to

All: 2 Fungi: 0 Insects: 0 Mammals: 2 Plants: 0

Items 1 - 2 of 2 One page.

☐ 1: [Cytochrome c oxidase subunit VIIa polypeptide 1 \(muscle\)](#)
COX7A1, *Homo sapiens*
Hs.421621: 264 sequences.
[Order cDNA clone](#)

☐ 2: [Cytochrome c oxidase subunit VIIa polypeptide 2 \(liver\)](#)
COX7A2, *Homo sapiens*
Hs.70312: 726 sequences.
[Order cDNA clone](#)

NCBI  **UniGene**
ORGANIZED VIEW OF THE TRANSCRIPTOME

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Limits Preview/Index History Clipboard Details

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dbEST
Trace Archive

NIH cDNA Projects
MGC | ZGC | XGC
Finding cDNAs

- Enter terms and click Preview to see only the number of search results.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

Search **Most Recent Queries**

#10 UniGene Links for OMIM (Select 123995)
#9 UniGene Links for OMIM (Select 123995)

Add Term(s) to Query or View Index:

- Enter a term in the text box; use the pull-down menu to specify a search field.
- Click Preview to add terms to the query box and see the number of search results, or click Index to view terms within a field.

Est Count 100:999999 Preview Index

Click AND OR NOT to add a term to the query box

NCBI UniGene

ORGANIZED VIEW OF THE TRANSCRIPTOME

Databases PubMed Nucleotide Protein Genome Structure

UniGene for 100:999999[Est Count]

Preview/Index History Clipboard Details

Summary Show 20 Sort by Organism

Aps.327: 148 sequences.

- 2: [Similar to heat shock cognate 70 protein](#)
LOC100159065, *Acyrrhosiphon pisum*
Aps.10: 135 sequences.
- 3: [Similar to tubulin alpha chain](#)
LOC100169457, *Acyrrhosiphon pisum*
Aps.128: 297 sequences.
- 4: [Similar to beta1-tubulin](#)
LOC100168148, *Acyrrhosiphon pisum*
Aps.278: 142 sequences.
- 5: [Similar to elongation factor 1-alpha](#)
LOC100165786, *Acyrrhosiphon pisum*
Aps.14665: 260 sequences.
- 6: [Actin](#)
LOC100145822, *Acyrrhosiphon pisum*
Aps.14735: 146 sequences.

1 of 3283 Next

Top Organisms [Tree]

- Homo sapiens (12488)
- Mus musculus (10468)
- Zea mays (3099)
- Bos taurus (2799)
- Danio rerio (2320)
- All other taxa (34482)

Recent activity

Turn Off Clear

- 100 : 999999[Est Count] (65656)
- Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
- UniGene Links for OMIM (S... (2) UniGene
- 123995 (4) OMIM
- Nucleotide Links for PopS... (170) Nucleotide

» See more...

NCBI UniGene

ORGANIZED VIEW OF THE TRANSCRIPTOME

UniGene Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search UniGene 0:999999[Est Count] Go Clear Save Search

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Show 20 Sort by Organism Send to

335 Mammals: 30054 Plants: 17266

Page 1 of 3283 Next

heavy chain
non pisum

heat 70 protein
non pisum

chain
non pisum

1: [Similar to heat shock cognate 70 protein](#)
LOC100168148, *Acyrrhosiphon pisum*
Aps.278: 142 sequences.

2: [Similar to tubulin alpha chain](#)
LOC100169457, *Acyrrhosiphon pisum*
Aps.128: 297 sequences.

3: [Similar to beta1-tubulin](#)
LOC100168148, *Acyrrhosiphon pisum*
Aps.278: 142 sequences.

4: [Similar to elongation factor 1-alpha](#)
LOC100165786, *Acyrrhosiphon pisum*
Aps.14665: 260 sequences.

5: [Actin](#)
LOC100145822, *Acyrrhosiphon pisum*
Aps.14735: 146 sequences.

Top Organisms [Tree]

- Homo sapiens (12488)
- Mus musculus (10468)
- Zea mays (3099)
- Bos taurus (2799)
- Danio rerio (2320)
- All other taxa (34482)

Recent activity

Turn Off Clear

- 100 : 999999[Est Count] (65656)
- Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
- UniGene Links for OMIM (S... (2) UniGene
- 123995 (4) OMIM
- Nucleotide Links for PopS... (170) Nucleotide

» See more...

NCBI **HomoloGene** *Discover Homologs* [Help](#)

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search HomoloGene for COX*[gene name]

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

HomoloGene is a system for automated detection of homologs among the annotated genes of several completely sequenced eukaryotic genomes.

HomoloGene Release 64 Statistics

Initial numbers of genes from complete genomes, numbers of genes placed in a homology group, and the numbers of groups for each species.

Species	Number of Genes		HomoloGene groups
	Input	Grouped	
Homo sapiens	22,165*	19,571	18,876
Pan troglodytes	25,096	17,243	16,375
Canis lupus familiaris	19,766	16,789	15,996
Bos taurus	22,049*	19,803	16,276
Mus musculus	25,388	21,786	19,026
Rattus norvegicus	21,991	19,267	17,512
Gallus gallus	17,959	13,207	11,969
Danio rerio	26,288	20,764	13,900
Drosophila melanogaster	14,085	9,315	7,796
Anopheles gambiae	12,460*	8,944	7,618
Caenorhabditis elegans	20,155*	8,685	4,829
Schizosaccharomyces pombe	5,043	3,237	2,949
Saccharomyces cerevisiae	5,880	4,854	4,373
Kluyveromyces lactis	5,335	4,462	4,385
Eremothecium gossypii	4,722	3,933	3,889
Magnaporthe grisea	12,832*	7,295	6,364

What's New

HomoloGene release 64 is now public. It includes updated annotations for the following species: Homo sapiens (NCBI release 37.1), Caenorhabditis elegans (WS190, NCBI release 8.1), Anopheles gambiae (AgamP3.3, NCBI release 3.1), Arabidopsis thaliana (NCBI release 8.1), Bos taurus (NCBI release 3.1), and Magnaporthe grisea (NCBI release 3.1).

Tip of The Day

You can use 'Details' in the tool bar to see how your query was translated and other query details. [\[More Tips\]](#)

NCBI **HomoloGene** *Discover Homologs* [Help](#)

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search HomoloGene for COX*[gene name] [Save Search](#)

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

Display Summary 20

All: 45 Fungi: 5 Mammals: 7

Items 1 - 20 of 45 Page 1 of 3 [Next](#)

☐ 1: HomoloGene:5017. Gene conserved in Eukaryota [Download](#)

LOC100289404	similar to Cytochrome c oxidase sub...	Homo sapiens
COX2	cytochrome c oxidase subunit II	Pan troglodytes
COX2	cytochrome c oxidase subunit II	Canis lupus familiaris
COX2	cytochrome c oxidase subunit II	Bos taurus
COX2	cytochrome c oxidase subunit II	Mus musculus
COX2	COXII	Rattus norvegicus
COX2	cytochrome c oxidase subunit II	Gallus gallus
COX2	cytochrome c oxidase subunit II	Danio rerio
COX2	cytochrome c oxidase subunit II	Drosophila melanogaster
COX2	cytochrome c oxidase subunit II	Anopheles gambiae
COX2	cytochrome c oxidase subunit II	Caenorhabditis elegans
cox2	cytochrome c oxidase 2	Schizosaccharomyces pombe
COX2	Cox2p	Saccharomyces cerevisiae
COX2	cytochrome c oxidase subunit 2	Kluyveromyces lactis
AGOS_AMI001W	AMI001Wp	Eremothecium gossypii
cox2	cytochrome c oxidase subunit 2	Arabidopsis thaliana
cox2	cytochrome c oxidase subunit 2	Oryza sativa

<input type="checkbox"/> 15: HomoloGene:36082	Gene conserved in Euteleostomi	Download
COX7A2	cytochrome c oxidase subunit VIIa p...	<i>Homo sapiens</i>
LOC738626	similar to cytochrome c oxidase sub...	<i>Pan troglodytes</i>
LOC611134	similar to cytochrome c oxidase, su...	<i>Canis lupus familiaris</i>
COX7A2	cytochrome c oxidase subunit VIIa p...	<i>Bos taurus</i>
Cox7a2	cytochrome c oxidase, subunit VIIa ...	<i>Mus musculus</i>
COX7A2	cytochrome c oxidase subunit VIIa p...	<i>Gallus gallus</i>
cox7a2	cytochrome c oxidase, subunit VIIa ...	<i>Danio rerio</i>

<input type="checkbox"/> 25: HomoloGene:48051	Gene conserved in Eutheria	Download
COX7A1	cytochrome c oxidase subunit VIIa p...	<i>Homo sapiens</i>
LOC612614	similar to Cytochrome c oxidase pol...	<i>Canis lupus familiaris</i>
COX7A1	cytochrome c oxidase subunit VIIa p...	<i>Bos taurus</i>
Cox7a1	cytochrome c oxidase, subunit VIIa ...	<i>Mus musculus</i>

[Discover Homologs](#)
[Help](#)

[All Databases](#)
[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[OMIM](#)
[PMC](#)
[Journals](#)
[Books](#)

Search HomoloGene for COX*[gene name] AND txid2759[Ancestor]
[Preview](#)
[Go](#)
[Clear](#)

[Limits](#)
[Preview/Index](#)
[History](#)
[Clipboard](#)
[Details](#)

[HomoloGene](#)
[Homepage](#)
[Query Tips](#)
[Build Procedure](#)
[FTP site](#)

[Genome](#)
[Resources](#)
[Homo sapiens](#)
[Mus musculus](#)
[Rattus norvegicus](#)
[Danio rerio](#)

- Enter terms and click Preview to see only the number of search results.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

Search

Most Recent Queries

[#13](#) Search COX*[gene name]
 [#12](#) Search 100:999999[Est Count]

Add Term(s) to Query or View Index:

- Enter a term in the text box; use the pull-down menu to specify a search field.
- Click Preview to add terms to the query box and see the number of search results, or click Index to view terms within a field.
- Multiple terms selected from Index will be ORed; click AND to add to search.

Ancestor

Preview
Index

Click **AND** **OR** **NOT** to add a term to the query box

txid186625 (606)
txid186626 (606)
txid186627 (606)
txid186634 (606)
txid197562 (1960)
txid197563 (1960)
txid207598 (990)
txid222514 (2009)
txid2759 (4158)
txid27592 (193)
txid28000 (193)

Up
Down

NCBI HomoloGene Discover Homologs

Search: HomoloGene for COX*[gene name] AND 'txid2759'(Ancestor) Go Clear Save Search

Limits: Summary Preview/Index History Clipboard Details

Display: Summary Show 20 Send to

Items 1 of 15

1: COX2 cytochrome c oxidase subunit II

2: COX2 cytochrome c oxidase subunit II

3: COX2 cytochrome c oxidase subunit II

4: COX2 cytochrome c oxidase subunit II

5: COX2 cytochrome c oxidase subunit II

6: COX2 cytochrome c oxidase subunit II

7: COX2 cytochrome c oxidase subunit II

8: COX2 cytochrome c oxidase subunit II

9: COX2 cytochrome c oxidase subunit II

10: COX2 cytochrome c oxidase subunit II

11: COX2 cytochrome c oxidase subunit II

12: COX2 cytochrome c oxidase subunit II

13: COX2 cytochrome c oxidase subunit II

14: COX2 cytochrome c oxidase subunit II

15: COX2 cytochrome c oxidase subunit II

Recent activity

COX*[gene name] AND 'txid...' (7)

COX*[gene name] (45)

100 : 999999(All Fields) (0)

100 : 999999(Est Count) (65656)

Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)

NCBI Entrez Taxonomy

Search: Taxonomy for Go Clear

Limits: Summary Preview/Index History Clipboard Details

Display: Summary Show 20 Send to

Items 1 - 15 of 15

1: Common Tree

2: LinkOut

3: Conserved Domain Links

4: 3D Domain Links

5: GEO DataSet Links

6: Gene Links

7: Genome Links

NCBI Taxonomy Browser

Enter name or id Add or Add from file: Browse... Choose subset Help

Expand All Collapse All Mark selected taxa Browse tree Delete taxa Save as text tree

Eukaryota

Plasmodium falciparum

Fungi/Metazoa group

Ascomycota

Schizosaccharomyces pombe

Saccharomycetaceae

Eremothecium gossypii

Kluyveromyces lactis

Saccharomyces cerevisiae

Bilateria

Caenorhabditis elegans

Coelomata

Amniota

Eutheria

Canis familiaris

Euarchontoglires

Murinae

Mus musculus

Rattus norvegicus

Homo/Pan/Gorilla group

Example1, Part III

NCBI

ENTREZ **SNP**
Single Nucleotide Polymorphism

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search for

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

Click on the image below to view the connections between Entrez SNP and other databases.

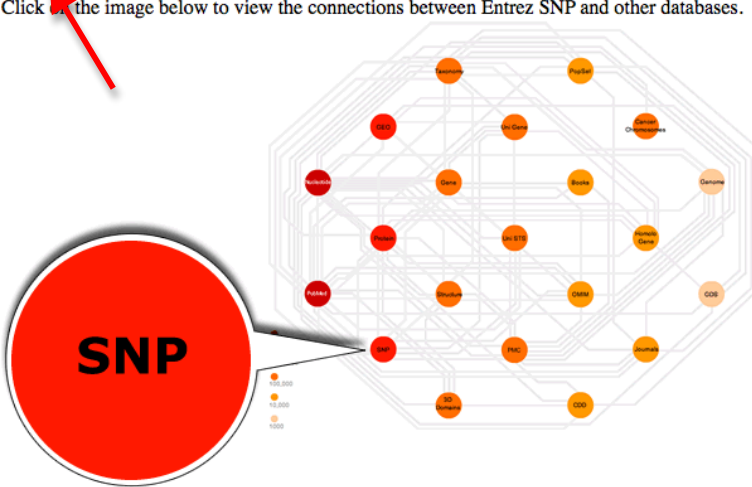
NCBI
dbSNP BUILD 131

Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel

My NCBI
My NCBI help

Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
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SNP

dbSNP is now incorporated into NCBI's Entrez system and can be queried using the same approach as the other Entrez and search options are available [here](#).

ENTREZ

SNP

Single Nucleotide Polymorphism

All DatabasesPubMedNucleotideProteinGenomeStructureOMIMPMCSNP Journals

Search SNP for
GoClear

LimitsPreview/IndexHistoryClipboardDetails

Limits: 22, snp_omim, snp_structure, nonsense, missense, frameshift, homo sapiens, 130

Limit your search by any of the following criteria.

OrganismCLEAR

☐ Anopheles gambiae
☐ Apis mellifera
☐ Bison bison
☐ Bos indicus x bos taurus
☐ Bos taurus
☐ Caenorhabditis elegans
☐ Canis familiaris
☐ Danio rerio
☐ Gallus gallus
☒ Homo sapiens
☐ Mus musculus

ChromosomesCLEAR

☐ 19
☐ 20
☐ 21
☒ 22
☐ 23
☐ 24
☐ 25
☐ 26
☐ 27
☐ 28
☐ 29

Chromosome RangeCLEAR

From:
To:

Map WeightCLEAR

☐ 1
☐ 2
☐ 3-10
☐ 10+

Function ClassCLEAR

☒ coding nonsynonymous
☒ nonsense
☒ missense
☒ frame shift
☐ intron
☐ coding synonymous
☐ locus region
☐ mrna utr
☐ 5' utr
☐ 3' utr
☐ splice site

SNP ClassCLEAR

☐ het
☐ in del
☐ microsatellite
☐ mixed
☐ mnp
☐ named
☐ no variation
☐ snp

AnnotationCLEAR

☒ Clinical/LSDB Submissions
☐ nucleotide
☐ OMIM
☐ protein
☐ structure
☐ PubMed
☐ Cited in PubMed

HeterozygosityCLEAR

☐ 0-10
☐ 40-50
☐ 10-20
☐ 20-30
☐ 30-40

Success RateCLEAR

☐ 80-85
☐ 85-90
☐ 90-95
☐ 95+

NCBI ENTREZ **SNP** Single Nucleotide Polymorphism

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search SNP for Go Clear Save Search

☒ Limits Preview/Index History Clipboard Details

Limits: 22, snp_gene_cmn, nonsense, missense, frameshift, homo sapiens

Display Graphic Summary Show 20 Sort By Send to

All: 27 1000 Genomes: 10 Cited in PubMed: 6 Clinical/LSDb Submissions: 27 Human: 27

Items 1 - 20 of 27 Page 1 of 2 Next

☐ 1: rs80358232 [Homo sapiens] Links

GGACCAAGACTACATCGTGGACCACT[C/T]CATTGCCATCTACCTGCTCAACCCCT

MapView VarView No PubMed GeneView Not on miRNA No 3D OMM

☐ 2: rs71799110 [Homo sapiens] Links

CACTCCTGTGGAGTTTATATCTG[C/G]GTGATTTTCAGGTGATTTCCTAA

MapView VarView No PubMed GeneView SeqView No 3D OMM

HGVS Names: [NM_001033024.1:c.895C>G] [NM_012179.3:c.1132C>G] [NP_001028196.1:p.Arg299Gly] [NP_036311.3:p.Arg378Gly] [NT_011520.12:g.12279825C>G]

☐ 3: rs61556467 [Homo sapiens] Links

CAACGGGCCGGAGGGCTGCATGGTGG[C/T]GGTGGCCACCTCACGCACTGAGAAG

MapView VarView No PubMed GeneView SeqView No 3D OMM

HGVS Names: [NG_008404.1:g.5340C>T] [NM_021076.3:c.269C>T] [NP_066554.2:p.Ala90Val] [NT_011520.12:g.9267089C>T]

☐ 4: rs60825978 [Homo sapiens] Links

AGCTGCTCGGCCAGATCCAGGGCTCC[A/G]GCGCCGCGCAGGCGCAGATGCAGGC

MapView VarView No PubMed GeneView SeqView No 3D OMM

HGVS Names: [NG_008404.1:g.5816G>A] [NM_021076.3:c.745G>A] [NP_066554.2:p.Gly249Ser] [NT_011520.12:g.9267565G>A]

☐ 5: rs59890097 [Homo sapiens] Links

AGGCCAAGTCCCAAGTGAAGGAAGAA[
- /GCCAAGTCCCAAGGAAG
]GCCAAGTCCCAAGGAAGCCAAAGA

NCBI ENTREZ **SNP** Single Nucleotide Polymorphism

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search SNP for Go Clear Save Search

Limits: 22, snp, gene, clin, nonsense, missense, frameshift, homo sapiens

Display UI List Show 20 Sort By Send to

All: 27 1000 Genomes: 10 Cited in PubMed: 6 Clinical/LSDb Submission an: 27

Items 1 - 20 of 27

- 1: [rs80358232](#) [Homo sapiens]
80358232
- 2: [rs71799110](#) [Homo sapiens]
71799110
- 3: [rs61556467](#) [Homo sapiens]
61556467
- 4: [rs60825978](#) [Homo sapiens]
60825978
- 5: [rs59890097](#) [Homo sapiens]
59890097
- 6: [rs59551486](#) [Homo sapiens]
59551486
- 7: [rs59371099](#) [Homo sapiens]

Entrez SNP
Search SNP
Search Mouse SNP
Common Query Filters
Entrez Batch Query
SNP Link Datamodel

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snp_result.txt

```

80358232
71799110
61556467
60825978
59890097
59551486
59371099
59297913
58099265
57188573
56940078
56916487
41302601
28941471
17883862
11568188
6010260
6006460
5763269
5830865
1135840
1065852
855791
738409
165602
140504
16947

```

NCBI

ENTREZ **SNP**
Single Nucleotide Polymorphism

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search for

Limits Preview/Index History Clipboard Details

Click on the image below to view the connections between Entrez SNP and other databases.

NCBI
dbSNP BUILD 131

Entrez SNP
Search SNP
Search Mouse SNP
Common Query Fields
Entrez Batch Query
SNP Link Datamodel

My NCBI
My NCBI help

Entrez SNP Help
Searchable FAQ
Search Fields
Programming Utilities
Batch Report
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dbSNP Home Page
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SNP

dbSNP is now incorporated into NCBI's Entrez system and can be queried using the same approach as the other Entrez and search options are available [here](#).

NCBI

Batch Entrez

All Databases PubMed Nucleotide Protein Genome Structure OMIM


Database File:


Batch Entrez


Use Batch Entrez to upload a file of GIs or accession numbers from the Nucleotide or Protein databases, or upload a list of record identifiers from other Entrez databases.

Tips : Some lists of record identifiers can be tens of thousands of lines long and Batch Entrez may not retrieve all records from one list. Split the list of identifiers into smaller files using a file splitting software or a file split command at the command prompt in UNIX or LINUX systems. Put several thousand record identifiers per file, left-formatted, and one per line. This may be necessary when you are loading large numbers of genome records. You can check the NCBI FTP site locations to download entire genome records. Also, use GIs rather than 'accession.version' numbers when making lists for batch entrez to fetch.

Received lines: 27
Rejected lines: 0
Removed duplicates: 0
Passed to Entrez: 27
[Retrieve records for 27 UID\(s\)](#)




















 **The NCBI C++ Toolkit [Internet]**
 Vakatov, Denis; Siyan, Karanjit; Ostell, James, editors.
 Bethesda (MD): [National Library of Medicine \(US\)](#), [NCBI](#); 2004 April

 **NCBI News**
 Bethesda (MD): [National Library of Medicine \(US\)](#), [NCBI](#); 2008

 **The NCBI Handbook**
 McEntyre, J.; Ostell, J., editors
 Bethesda (MD): [National Library of Medicine \(US\)](#), [NCBI](#); 2002-2005

 **NCBI Help Manual**
 Bethesda (MD): [National Library of Medicine \(US\)](#), [NCBI](#); 2005-2009

 **NCBI Short Courses**
 Airozo, Diana; Al-Ubaydli, Mohammad; Sayers, Eric; Wheeler, David
 Bethesda (MD): [National Library of Medicine \(US\)](#), [NCBI](#); 2004

Example 2:

I. PubMed, PMC, Taxonomy and PopSet

Besides mammoth, how many other extinct organisms have data available in the Entrez databases? Go to the Preview/Index of the Taxonomy database, select the “Properties” field and from its index “Extinct”. These records can be combined with the “Filter” that limits the search to those taxonomy records that have links to PubMed Central (PMC). The resulting search phrase: "extinct"[Properties] AND "taxonomy pmc"[Filter] Select the *Emeus crassus* entry. What is the origin of eastern moa’s specimens that have their sequences reported in the Entrez databases? What is the lineage for this organism? Link to the PMC database and access the publication on giant moas. Link to full text of the article published by Baker et al.. Navigate to Fig 2 in the Results and Discussion section, if you are interested in the appearance of these extinct birds.

Return to Taxonomy and from there link to the PopSet database. In the record submitted by Lambert DM, several ancient organisms were compared. Which gene was used in the sequence comparison? From the PopSet record link to the Nucleotide database. List all the organisms studied in this set (hint: use “Sort by TaxID”). Select the *Emeus crassus* and *Dinornis robustus* nucleotide records and temporarily save them on the Clipboard.

II. OMIM, UniGene and Homologene

Perform an unlimited search for records relating to cholesterol transport in the OMIM database. Repeat the query for “cholesterol transport” as a term. Which search is more restrictive? Limit the retrieved entries only to those with gene location on chromosome 22. How many records have you retrieved? What is the chromosomal location of the gene APOL1 (OMIM record 603743)? How many APOL genes are clustered on chromosome 22? From the APOL1 OMIM record link to the UniGene database. Compare the expression profiles of the APOL1 and APOL2 genes focusing on the developmental stage. What do you conclude from the expression profiles? Perform a search for those UniGene records that are expressed in neonates (use the following: "neonate"[Expression]). Combine the result of the search with the six records that you have obtained through the OMIM link. Which members of the APOL gene family have no expression in neonates? Is the evidence strong for all of them? Search the HomoloGene database for records relating to APO genes (Preview/Index—Gene Name). How many records have you retrieved? Are all apolipoprotein genes equally conserved in evolution? What are their common ancestors? Which of these genes are conserved in placental mammals (Eutheria, Taxonomy ID 9347). Display the taxonomy tree for organisms included in the record containing human APOL6 homologs.

III. dbSNP

Access the SNP database and select its Limits page. Check the appropriate boxes to allow selection for SNPs at the splice site of human chromosome 22. Sort the list by organism. Retrieve and download the UI List for these records. Use the saved file to retrieve the records with the UI List in Batch Entrez.